



TTTGTGGAGGGCAGACAGAGAGTACCCAGCTGGACATCCTTTCTGCTGATGAGCCAGGTCGCCCTGCTCATGCTCTTCCC  
90  
AAACACCTCCCGTCGCTCTCATGGGTCGACCTGTAGGAAAGGACGACTACTCGGGGTCCGACCTCCACGGGACGAGTGACGAGAAGGG

M S P R L E V P C S H A L P

CAGGGTCTCTCGCCTGGGCAGGTCATCATAGTACGGGGACTGGTCTTGCAAGAGCCGAAGCATTTTACTGTGAGCCTGAGGGACCAGGCT  
180  
GTCCCAGAGAGCGGACCCGTCCAGTAGTATCATGCCCTGACCAGAACGTTCTCGGCTTCGTAAAATGACACTCGGACTCCCTGGTCCGA

Q G L S P G Q V I I V R G L V L Q E P K H F T V S L R D Q A

GCCCATGCTCCTGTGACACTCAGGGCCTCCTTCGCAGACAGAACTCTGGCCTGGATCTCCCGCTGGGGGCAGAAGAACTGATCTCAGCC  
270  
CGGGTACGAGGACACTGTGAGTCCCGGAGGAAGCGTCTGTCTTGAGACCGGACCTAGAGGGCGACCCCCGTCTTCTTTGACTAGAGTCGG

A H A P V T L R A S F A O R T L A W I S R W G Q K K L I S A

CCCTTCCTCTTTTTACCCCCAGAGATTCTTTGAGGTGCTGCTCCTGTTCCAGGAGGGAGGGCTGAAGCTGGCGCTCAATGGGCAGGGGCTG  
360  
CGAAGGAGAAAAATGGGGGTCTCTAAGAACTCCACGACGAGGACAAGGTCTCCCTCCCGACTTCGACCGCGAGTTAECGTCCCCGAC

F L F Y P Q R F F E V L L L F Q E G G L K L A L N G Q G L

GGGGCCACCAGCATGAACCAGCAGGCCCTGGAGCAGCTGCGGGAGCTCCGGATCAGTGGAAGTGTCAGCTCTACTGTGTCCACTCCTGA  
450  
CTCCGGTGGTCTGTA CT TGGTCTCGTCCGGGACCTCGTCGACGCCCTCGAGGCCTAGTCACCTTCACAGGTCGAGATGACACAGGTGAGGACT

"G A T S M N Q Q A L E Q L R E L R I S G S V Q L Y C V H S .

AGATGGTTCCAGGAAATACCGCAGAAAAACAAGAGTCAGCCACTCCCCAGGGCCCCACTCTCCTCCCTCATTAAACCATCCACCTGAAC  
540  
TCTACCAAGGTCCTTTATGGCGTCTTTTGTCTCAGTCGGTGAGGGGTCCCGGGGTGAGAGGAGGGGAGTAATTTGGTAGGTGGACTTG

ACCAGCACATCAGGGCCTGGTTCACCTCTGGGGTCACGAGACTGAGTCTACAGGAGCTTTGGGCCTGAGGGAAGGCACAAGAGTGCAAAG  
630  
TGGTCGTGTAGTCCCGGACCAAGTGAGACCCAGTGCTCTGACTCAGATGTCTCGAAACCCGGACTCCCTTCCGTGTTCTCACGTTTC

GTTCTCGAACTCTGCACCTTCCTCCACCAGGAGCCTGGGATATGGCTCCATCTGCCTTCAGGGCCTGGACTGCACTCACAGAGGCAAGT  
720  
CAAGGAGCTTGAGACGTGGAAGGAGGTGGTCTCGGACCCTATACCGAGGTAGACGGAAGTCCCGGACCTGACGTGAGTGCTCCGTTC

GTTGTAGACTAACAAAGATACTCCAAAATACAATGGCTTAAAGAATGTGGTCATTTATTCTTTATTATTTATTTATTTGTGGTCAAATAA  
810  
CAACATCTGATTGTTTCTATGAGGTTTTATGTTACCGAATTTCTTACACCAGTAAATAAGAAATAATAAATAAATAAACCACAGTTTATT

ATAAATAAGGTTATTTATTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
865  
TATTTATTTCCAATAAATAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT

FIGURE 2

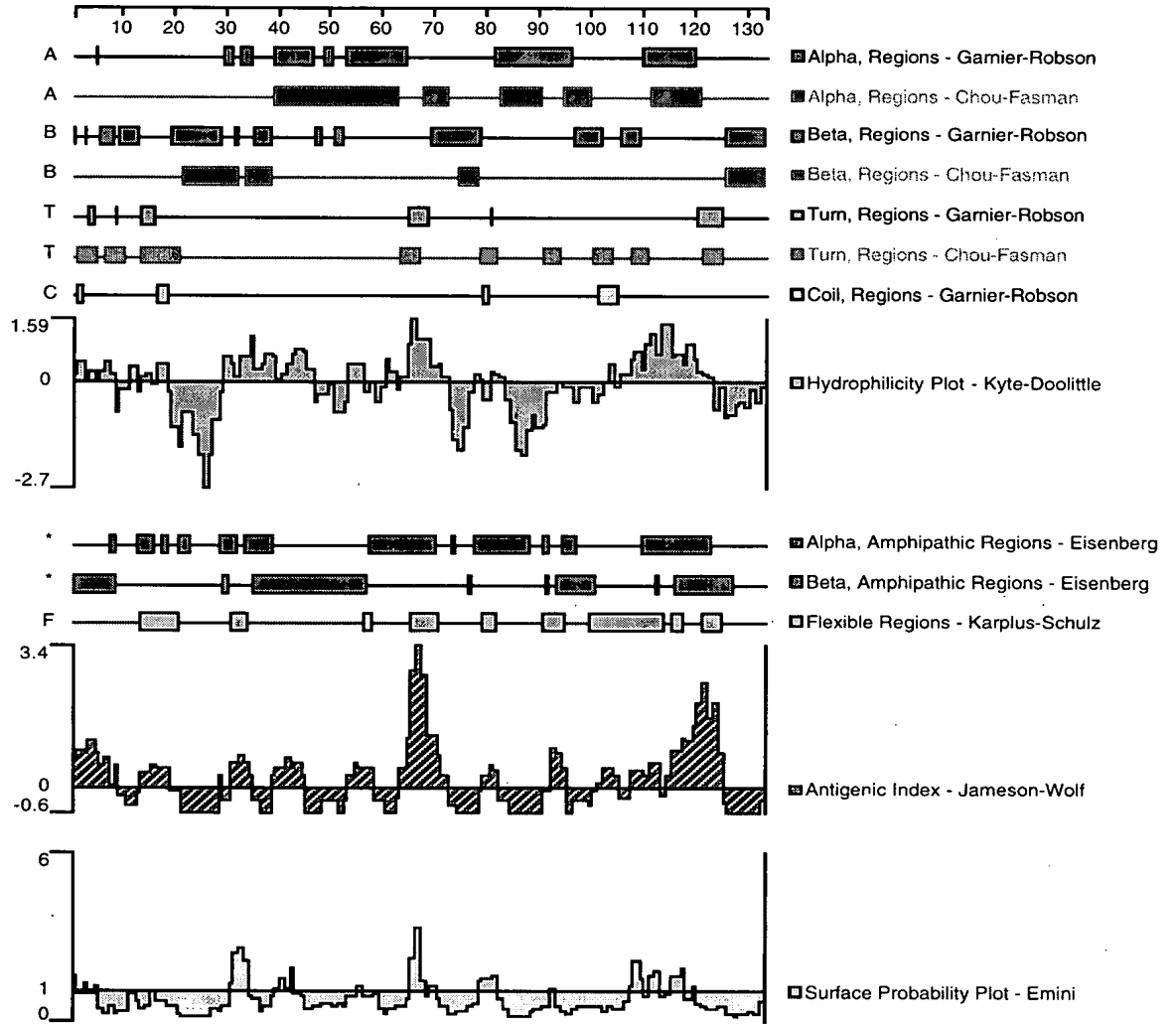
		10		20		30		40																																			
1	M	S	-	-	-	-	-	-	P	R	L	E	-	-	-	-	-	-	V	P	C	S	H	A	L	P	Q	G	L	S	P	G	Q	V	HJACE54.aa								
1	M	S	S	F	S	T	Q	T	P	Y	P	N	L	A	-	-	-	-	-	V	P	F	F	T	S	I	P	N	G	L	Y	P	S	K	S	rGalectin-5.aa							
1	M	M	-	-	-	-	-	-	-	-	L	S	L	N	N	L	Q	N	I	I	Y	N	P	V	I	P	F	V	G	T	I	P	D	Q	L	D	P	G	T	L	hGalectin-8.aa		

Decoration 'Decoration #1': Box residues that match the consensus named 'Consensus #2' exactly.

Decoration 'Decoration #2': Shade (with solid black) residues that match the consensus named 'Consensus #1' exactly.

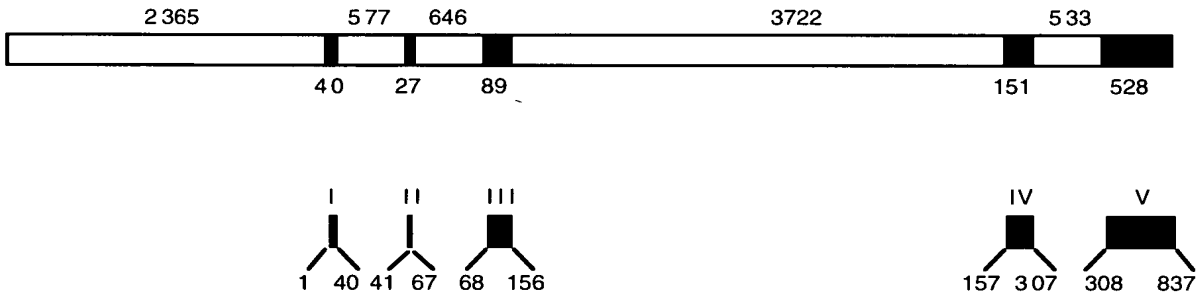
09109864.070698

FIGURE 3



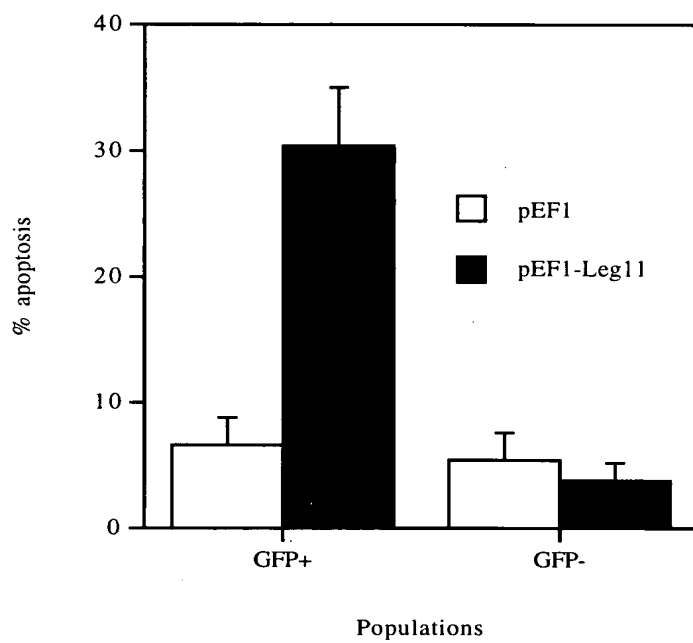
09109864.070698

FIGURE 4



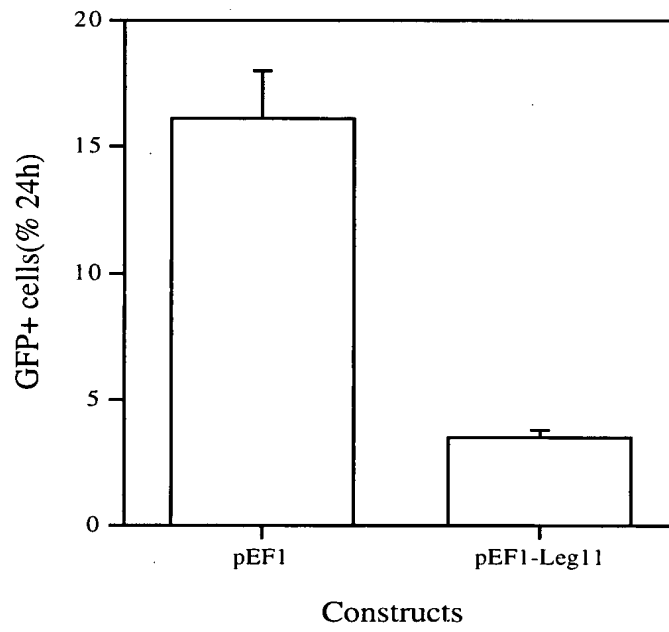
065020"49860760

FIGURE 5A



09109864-070698  
859020-19860760

FIGURE 5B



869020"49860160